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TECH CENTER 1600/2900

SEQUENCE LISTING

<110> Grainger, David J.
Tatalick, Lauen Marie

<120> Compounds and methods to inhibit or
augment an inflammatory response.

<130> 1543.001US1

<140> US 08/927939

<141> 1997-09-11

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<211> 12

<212> PRT

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
1 5 10 15

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<211> 15

<212> PRT

<213> Homo sapiens

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His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
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<211> 14

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<213> Homo sapiens

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Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val
1 5 10

<210> 6

<211> 15

<212> PRT

<213> Homo sapiens

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Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu
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<211> 10

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<213> Homo sapiens

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Cys Ala Asp Pro Lys Gln Lys Trp Val Gln
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<210> 8

<211> 6

<212> PRT

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<400> 8

Glu Ile Cys Ala Asp Pro
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<213> Homo sapiens

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1 5 10

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<213> Homo sapiens

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<213> Homo sapiens

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Glu Ile Cys Leu Asp Pro Lys Gln Lys Trp Ile Gln
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<210> 15

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<212> PRT

<213> Homo sapiens

<400> 15

Cys Pro Ser Leu Glu Asp Ser Phe Ile Gln Val Ala
1 5 10

<210> 16

<211> 99

<212> PRT

<213> Homo sapiens

<400> 16

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
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20 25 30
Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
35 40 45
Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
50 55 60
Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
65 70 75 80
Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
85 90 95
Pro Lys Thr

<210> 17

<211> 77

<212> PRT

<213> Homo sapiens

<400> 17

Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val
1 5 10 15
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20 25 30
Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg
35 40 45
Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser
50 55 60
Met Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
65 70 75

<210> 18
<211> 99
<212> PRT
<213> Homo sapiens

Put G1
<400> 18
Met Lys Ala Ser Ala Ala Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala
1 5 10 15
Phe Ser Pro Gln Gly Leu Ala Gln Pro Val Gly Ile Asn Thr Ser Thr
20 25 30
Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu
35 40 45
Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg Glu Ala Val
50 55 60
Ile Phe Lys Thr Lys Leu Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
65 70 75 80
Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
85 90 95
Pro Lys Leu

<210> 19
<211> 92
<212> PRT
<213> Homo sapiens

<400> 19
Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
1 5 10 15
Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
20 25 30
Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
35 40 45
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
50 55 60
Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
65 70 75 80
Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala
85 90

<210> 20
<211> 92
<212> PRT
<213> Homo sapiens

<400> 20
Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
1 5 10 15
Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
20 25 30
Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
35 40 45
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
50 55 60
Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
65 70 75 80
Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
85 90

<210> 21
<211> 91
<212> PRT

<213> Homo sapiens

<400> 21

Met Lys Val Ser Ala Ala Arg Leu Ala Val Ile Leu Ile Ala Thr Ala
1 5 10 15
Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
20 25 30
Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
35 40 45
Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
50 55 60
Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
65 70 75 80
Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
85 90

<210> 22

<211> 89

<212> PRT

<213> Homo sapiens

<400> 22

Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
1 5 10 15
Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
20 25 30
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
35 40 45
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
50 55 60
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
65 70 75 80
Glu Tyr Leu Glu Lys Ala Leu Asn Lys
85

<210> 23

<211> 99

<212> PRT

<213> Homo sapiens

<400> 23

Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
1 5 10 15
Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
20 25 30
Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
35 40 45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
50 55 60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
65 70 75 80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
85 90 95
Glu Asn Ser

<210> 24

<211> 107

<212> PRT

<213> Homo sapiens

<400> 24

Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15
 Arg Val Ala Leu Leu Leu Leu Leu Val Ala Ala Gly Arg Arg Ala
 20 25 30
 Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35 40 45
 Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
 50 55 60
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65 70 75 80
 Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
 85 90 95
 Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
 100 105

<210> 25
 <211> 97
 <212> PRT
 <213> Homo sapiens

<400> 25
 Met Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala
 1 5 10 15
 Phe Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys
 20 25 30
 Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser
 35 40 45
 Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe
 50 55 60
 Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp
 65 70 75 80
 Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys
 85 90 95
 Pro

<210> 26
 <211> 148
 <212> PRT
 <213> Mus musculus

<400> 26
 Met Gln Val Pro Val Met Leu Leu Gly Leu Leu Phe Thr Val Ala Gly
 1 5 10 15
 Trp Ser Ile His Val Leu Ala Gln Pro Asp Ala Val Asn Ala Pro Leu
 20 25 30
 Thr Cys Cys Tyr Ser Phe Thr Ser Lys Met Ile Pro Met Ser Arg Leu
 35 40 45
 Glu Ser Tyr Lys Arg Ile Thr Ser Ser Arg Cys Pro Lys Glu Ala Val
 50 55 60
 Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala Asp Pro Lys Lys
 65 70 75 80
 Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg Asn Gln Met Arg
 85 90 95
 Ser Glu Pro Thr Thr Leu Phe Lys Thr Ala Ser Ala Leu Arg Ser Ser
 100 105 110
 Ala Pro Leu Asn Val Lys Leu Thr Arg Lys Ser Glu Ala Asn Ala Ser
 115 120 125
 Thr Thr Phe Ser Thr Thr Thr Ser Ser Thr Ser Val Gly Val Thr Ser
 130 135 140
 Val Thr Val Asn
 145

<210> 27
<211> 10
<212> PRT
<213> Homo sapiens

<400> 27
Cys Leu Asp Pro Lys Lys Glu Trp Ile Gln
1 5 10

<210> 28
<211> 825
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (34) ... (327)

<400> 28

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Met Lys Val Ser Ala Val Leu
1 5

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Leu Cys Leu Leu Leu Met Thr Ala Ala Phe Asn Pro Gln Gly Leu Ala
10 15 20

cag cca gat gca ctc aac gtc cca tct act tgc tgc ttc aca ttt agc 150
Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser
25 30 35

agt aag aag atc tcc ttg cag agg ctg aag agc tat gtg atc acc acc 198
Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
40 45 50 55

agc agg tgt ccc cag aag gct gtc atc ttc aga acc aaa ctg ggc aag 246
Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
60 65 70

gag atc tgt gct gac cca aag gag aag tgg gtc cag aat tat atg aaa 294
Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys
75 80 85

cac ctg ggc cgg aaa gct cac acc ctg aag act tgaactctgc taccctact 347
His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
90 95

gaaatcaagc tggagtacgt gaaatgactt ttccattctc ctctggcctc ctcttctatg 407
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gtactatgtg ttaagtaata ttggctatta ttgacttgt tgctggtttg gagtttattt 527
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<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (80) ... (358)

<400> 29

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ccgccccgcc gcccgccc atg aac gcc aag gtc gtg gtc gtg ctg gtc ctc 112
Met Asn Ala Lys Val Val Val Val Leu Val Leu
1 5 10

gtg ctg acc gcg ctc tgc ctc agc gac ggg aag ccc gtc agc ctg agc 160
Val Leu Thr Ala Leu Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser
15 20 25

tac aga tgc cca tgc cga ttc ttc gaa agc cat gtt gcc aga gcc aac 208
Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn
30 35 40

gtc aag cat ctc aaa att ctc aac act cca aac tgt gcc ctt cag att 256
Val Lys His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile
45 50 55

gta gcc cgg ctg aag aac aac aac aga caa gtg tgc att gac ccg aag 304
Val Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
60 65 70 75

cta aag tgg att cag gag tac ctg gag aaa gct tta aac aag agg ttc 352
Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe
80 85 90

aag atg tgagagggtc agacgcctga ggaaccctta cagtaggagc ccagctctga 408
Lys Met

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Ref 61

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<210> 30
 <211> 4259
 <212> DNA
 <213> Mus musculus

<220>
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 <222> (2070) ... (2130)

<221> CDS
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Sub 61

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tgagtcattc	ccaaagtcag	ccaatcagga	ctcagggagg	gaaactcttt	gcagataaat	1980
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aaccttcggt	aagcctcccc	atcagcacc	atg aac cca	agt gct gcc gtc att		2093

Met	Asn	Pro	Ser	Ala	Ala	Val	Ile
1				5			

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Phe	Cys	Leu	Ile	Leu	Leu	Gly	Leu	Ser	Gly	Thr	Gln			
10						15					20			

ccaaggccat	ttaattaacg	aagtcagaag	tcagacgatt	aagctcagtt	ctaaacacag	2200
catgtattta	agctttaatg	tgtgtacctt	taaagaagag	ggaagcagga	agaaatccct	2260
tcagcttgca	gagttttatc	taggctgggt	gaagtcagag	aaaaatagaa	taaaagaaaa	2320
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atctctcttt	accatgacca	agatattcaa	acactcagcc	ctatgatacg	atgggatgcg	2560
tctctccaca	gatcagacag	ggctctgctaa	acactacctc	atccatttta	agtgcctaaa	2620
atgaaaccgt	gtgctgacct	tcctggctct	ccccctctct	tcctgcag	gg atc cct	2676

Gly Ile Pro

ctc	gca	agg	acg	gtc	cgc	tgc	aac	tgc	atc	cat	atc	gat	gac	ggg	cca	2724
Leu	Ala	Arg	Thr	Val	Arg	Cys	Asn	Cys	Ile	His	Ile	Asp	Asp	Gly	Pro	
25						30					35					

gtg	aga	atg	agg	gcc	ata	ggg	aag	ctt	gaa	atc	atc	cct	gcg	agc	cta	2772
Val	Arg	Met	Arg	Ala	Ile	Gly	Lys	Leu	Glu	Ile	Ile	Pro	Ala	Ser	Leu	
40					45				50				55			

tcc	tgc	cca	cgt	gtt	gag	atc	at	gtgagtacaa	gcccacctgc	cgataaacgt	2825
Ser	Cys	Pro	Arg	Val	Glu	Ile	Ile				
				60							

ccctcccgtg	accacacagt	aaataagtga	gggaaaccag	gaaagatggg	gacgggtctg	2885
tgactctaac	taaggcacag	tgctgaact	ctgacatgga	cctgcagggc	catcagctct	2945
gttggcctga	cgtaaatctg	agtatctcac	tcttatttct	atag t gcc	acg atg	2999

Ala Thr Met
65

aaa	aag	aat	gat	gag	cag	aga	tgt	ctg	aat	ccg	gaa	tct	aag	acc	atc	3047
Lys	Lys	Asn	Asp	Glu	Gln	Arg	Cys	Leu	Asn	Pro	Glu	Ser	Lys	Thr	Ile	
		70						75					80			

aag	aat	tta	atg	aaa	gcg	ttt	agc	caa	aaa	ag	gtaggtttga	tgttgctttt	3099
Lys	Asn	Leu	Met	Lys	Ala	Phe	Ser	Gln	Lys	Arg			
		85				90							

tcaggaaatg	gtgggtctggg	gagcagcgcc	tgccctgggc	tttgctgtgg	gcattctgcc	3159
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taaactcatg gcaccggcat gtgcctttgt ctctccattt acacagacac tgaggtgcct 3219
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 ggaaaatgca ccaggcctt tgecccaggg tctttgggtt ccaaagtga agcagagtct 3459
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Ser Lys Arg Ala Pro

95

taactggaga gaagccacgc acacaccccg gtgctgtgat ggacagcaga gagcctgtct 3566
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 aatgggtagt taaagtttat ttttaaaacc gtccaatacc ttttgtatta tgtaacattc 4166
 aaaagacaat gtactgtatt gaaagttagta agagacccaa aatgtaataa agtaataata 4226
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<210> 31

<211> 1081

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (43) ... (363)

<400> 31

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 Met Ala Arg Ala
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acg ctc tcc gcc gcc ccc agc aat ccc cgg ctc ctg cgg gtg gcg ctg 102
 Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu Arg Val Ala Leu
 5 10 15 20

ctg ctc ctg ctc ctg gtg gcc gcc agc cgg cgc gca gca gga gcg ccc 150
 Leu Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala Ala Gly Ala Pro
 25 30 35

ctg gcc act gaa ctg cgc tgc cag tgc ttg cag acc ctg cag gga att 198
 Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr Leu Gln Gly Ile
 40 45 50

cac ctc aag aac atc caa agt gtg aag gtg aag tcc ccc gga ccc cac 246
 His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser Pro Gly Pro His
 55 60 65

tgc gcc caa acc gaa gtc ata gcc aca ctc aag aat ggg cag aaa gct 294
 Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn Gly Gln Lys Ala
 70 75 80

tgt ctc aac ccc gca tgc ccc atg gtt aag aaa atc atc gaa aag atg 342
 Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile Ile Glu Lys Met
 85 90 95 100

ctg aaa aat ggc aaa tcc aac tgaccagaag gaaggaggaa gcttattggg 393

Leu Lys Asn Gly Lys Ser Asn

105

ggctgttccct gaaggaggcc ctgcccttac aggaacagaa gaggaagag agacacagct 453
 gcagaggcca cctggattgc gcctaattgtg tttgagcatc acttaggaga agtcttctat 513
 ttattttattt attttatttat ttgtttgttt tagaagattc tatgtttaata ttttatgtgt 573
 aaaataaggt tatgattgaa tctacttgca cactctccca ttatatttat tgtttatttt 633
 aggtcaaacc caagttagtt caatcctgat tcatatttaa tttgaagata gaaggtttgc 693
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 tgcagtgttt ccctctgtgt tagagcagag aggtttcgat atttattgat gttttcacaa 1053
 agaacaggaa aataaaatat ttaaaaat 1081

<210> 32

<211> 1173

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (107) ... (448)

<400> 32

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 cccagttcag gaaccgcgca ccgctcgcag cgctctcttg accact atg agc ctc 115
 Met Ser Leu
 1

ctg tcc agc cgc gcg gcc cgt gtc ccc ggt cct tcg agc tcc ttg tgc 163
 Leu Ser Ser Arg Ala Ala Arg Val Pro Gly Pro Ser Ser Ser Leu Cys
 5 10 15

gcg ctg ttg gtg ctg ctg ctg ctg ctg acg cag cca ggg ccc atc gcc 211
 Ala Leu Leu Val Leu Leu Leu Leu Leu Thr Gln Pro Gly Pro Ile Ala
 20 25 30 35

agc gct ggt cct gcc gct gct gtg ttg aga gag ctg cgt tgc gtt tgt 259
 Ser Ala Gly Pro Ala Ala Ala Val Leu Arg Glu Leu Arg Cys Val Cys
 40 45 50

tta cag acc acg cag gga gtt cat ccc aaa atg atc agt aat ctg caa 307
 Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser Asn Leu Gln
 55 60 65

gtg ttc gcc ata ggc cca cag tgc tcc aag gtg gaa gtg gta gcc tcc 355
 Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val Val Ala Ser
 70 75 80

ctg aag aac ggg aag gaa att tgt ctt gat cca gaa gcc cct ttt cta 403
 Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu
 85 90 95

aag aaa gtc atc cag aaa att ttg gac ggt gga aac aag gaa aac 448
 Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys Glu Asn
 100 105 110

tgattaagag aaatgagcac gcatggaaaa gtttccagct ctacagcaga gaagttttct 508
 ggaggtctct gaaccaggg aagacaagaa ggaaagattt tgttggtgtt tgtttatttg 568
 gtttccccag tagttagctt tcttccctgg attcctcact tttgaagagt gtgaggaaaa 628

cctatgtttg ggcgttaagc tttcagctca gcttaaatgaa gtgttttagca tagtacctct 688
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 tgggaaatat tttaatgttt cttgggggaat atgttagaga attcccttac tcttgattgt 988
 gggatactat ttaattattt cacttttagaa agctgagtgt ttcacacctt atctatgtag 1048
 aatatatttc cttattcaga atttctaaaa gtttaagttc tatgagggct aatatcttat 1108
 cttcctataa ttttagacat tgctttaact ttttagtaaa aaaaaaaaaa aaaaaaaaaa 1168
 aaaaa 1173

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 <211> 825
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (34)...(327)

<400> 33
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 Met Lys Val Ser Ala Val Leu
 1 5
 ctg tgc ctg ctg ctc atg aca gca gct ttc aac ccc cag gga ctt gct 102
 Leu Cys Leu Leu Leu Met Thr Ala Ala Phe Asn Pro Gln Gly Leu Ala
 10 15 20
 cag cca gat gca ctc aac gtc cca tct act tgc tgc ttc aca ttt agc 150
 Gln Pro Asp Ala Leu Asn Val Pro Ser Thr Cys Cys Phe Thr Phe Ser
 25 30 35
 agt aag aag atc tcc ttg cag agg ctg aag agc tat gtg atc acc acc 198
 Ser Lys Lys Ile Ser Leu Gln Arg Leu Lys Ser Tyr Val Ile Thr Thr
 40 45 50 55
 agc agg tgt ccc cag aag gct gtc atc ttc aga acc aaa ctg ggc aag 246
 Ser Arg Cys Pro Gln Lys Ala Val Ile Phe Arg Thr Lys Leu Gly Lys
 60 65 70
 gag atc tgt gct gac cca aag gag aag tgg gtc cag aat tat atg aaa 294
 Glu Ile Cys Ala Asp Pro Lys Glu Lys Trp Val Gln Asn Tyr Met Lys
 75 80 85
 cac ctg ggc cgg aaa gct cac acc ctg aag act tgaactctgc taccctact 347
 His Leu Gly Arg Lys Ala His Thr Leu Lys Thr
 90 95
 gaaatcaagc tggagtacgt gaaatgactt ttccattctc ctctggcctc ctcttctatg 407
 ctttgaata cttctaccat aattttcaaa taggatgcat tcggttttgt gattcaaaat 467
 gtactatgtg ttaagtaata ttggctatta tttgaattgt tgctggtttg gagtttattt 527
 gagtattgct gatcttttct aaagcaaggc cttgagcaag taggttgctg tctctaagcc 587
 ccttccctt ccactatgag ctgctggcag tgggttgat tcggttccca ggggttgaga 647
 gcatgcctgt gggagtcag gacatgaagg gatgctgcaa tgtaggaagg agagctcttt 707
 gtgaatgtga gggtgttgct aaattattgt ttattgtgga aagatgaatg caatagtagg 767
 actgctgaca ttttgagaa aatacathtt atttaaaate tcctaaaaaa aaaaaaaaaa 825

<210> 34
 <211> 3112
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (1192) ... (1267)

<221> CDS
<222> (1953) ... (2067)

<221> CDS
<222> (2488) ... (2575)

<400> 34

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atggctccat atttgggttg tttccacaga actctttccc agaaatgctt tttctagggtt 180
aatggctaca catatttcta ggcacctgac atactgacac ccacctctaa agtattttta 240
tgatccacaa cttagcgtta acacagcgcc ccagtcactc cgagactaat aaatagacaa 300
atgactgaaa cgtgacctca tgctttctat tctctcagct ttcattgagt tcttttctc 360
tgggaggact gggggttctc tagccctcca cagcatcagc ccattgacct tatccttggtg 420
gttatagcag ctgaggaagc agaattacag ctctgtggga aggaatgggg ctggagaggtt 480
catgcataga ccaattcttt tttttttttt tttttgagat ggagtttcac ttttgttgcc 540
caggctggag tgcaatggca tgatctcagc tcaccacagc cccacctcc tgggttcaag 600
cgattctcct gccctcagcc tcccagtag ctgggattac aggcattgtgc caccacgcct 660
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acttaaaaat ttcctctctc acccccagat tccatttccc catccgccag ggctgcctat 1080
aaagaggaga gatggcttca gacatcagaa ggacgcaggc agcaaagagt agtcagtcctc 1140
ttcttggctc tgctgacact cgagcccaca ttccatcacc tgctcccaat c atg cag 1197
Met Gln
1

gtc tcc act gct gcc ctt gcc gtc ctc ctc tgc acc atg gct ctc tgc 1245
Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala Leu Cys
5 10 15

aac cag gtc ctc tct gca cca c gtgagtcctat gttgttggtt tgggtatcac 1297
Asn Gln Val Leu Ser Ala Pro
20 25

cactctctgg ccatgggttag accacatcag tctttttttg cggcctgaga gccccgaaga 1357
gaaaagaagg aagttcttaa agcgtgcca aacaccttgg tctttttctt cacaactttt 1417
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ccttgtagtc acttggtctg agcaagcctg ccctcctcaa ccactcaggg atcagaagct 1897
gcctggcctt ttcttctgag ctgtgactcg ggcttattct ctcctttctc cgcag tt 1954
Leu

gct gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cga cag 2002
Ala Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln
30 35 40

att cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc 2050
Ile Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys

45

50

55

tcc aag ccc agt gtc at gtaagtgccg gtcttctctg tcacctctag
 Ser Lys Pro Ser Val Ile
 60

2097

ggaggtaggg agtgtcaggg tgggggcaga aacaggccag aaggccatcc tggaaaggcc 2157
 cagccttcag gacgctatcg gggatacagg acgcagggca ctgaggtgtg acctgacttg 2217
 gggctggagt gaggtgggtg ttacagagtc aggaagggtc gcccaggcc agaggaaagg 2277
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 aagctctcta gacggagata ggcagggggc ccctgagaga ggagcaggcc ttgagctgcc 2397
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 Phe Leu Thr Lys Arg Gly Arg
 65 70

cag gtc tgt gct gac ccc agt gag gag tgg gtc cag aaa tac gtc agt 2557
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser
 75 80 85

gac ctg gag ctg agt gcc tgaggggtcc agaagcttcg agggccagcg 2605
 Asp Leu Glu Leu Ser Ala
 90

acctcagtgg gcccagtggg gaggagcagg agcctgagcc ttgggaacat gcggtgtgacc 2665
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 aataataaag atgttctttt aaacggtaaa ccagtattga gtttggtttt gtttttctgg 3025
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<210> 35

<211> 481

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55) ... (333)

<400> 35

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 Met
 1

aag atc tcc gtg gct gcc att ccc ttc ttc ctc ctc atc acc atc gcc 105
 Lys Ile Ser Val Ala Ala Ile Pro Phe Phe Leu Leu Ile Thr Ile Ala
 5 10 15

cta ggg acc aag act gaa tcc tcc tca cgg gga cct tac cac ccc tca 153
 Leu Gly Thr Lys Thr Glu Ser Ser Ser Arg Gly Pro Tyr His Pro Ser
 20 25 30

gag tgc tgc ttc acc tac act acc tac aag atc ccg cgt cag cgg att 201
 Glu Cys Cys Phe Thr Tyr Thr Thr Tyr Lys Ile Pro Arg Gln Arg Ile
 35 40 45

atg gat tac tat gag acc aac agc cag tgc tcc aag ccc gga att gtc 249
 Met Asp Tyr Tyr Glu Thr Asn Ser Gln Cys Ser Lys Pro Gly Ile Val

50

55

60

65

ttc atc acc aaa agg ggc cat tcc gtc tgt acc aac ccc agt gac aag 297
 Phe Ile Thr Lys Arg Gly His Ser Val Cys Thr Asn Pro Ser Asp Lys
 70 75 80

tgg gtc cag gac tat atc aag gac atg aag gag aac tgagtgaccc 343
 Trp Val Gln Asp Tyr Ile Lys Asp Met Lys Glu Asn
 85 90

agaaggggtg gcgaaggcac agctcagaga cataaagaga agatgccaaag gccccctcct 403
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 agaccactca tgctcttc 481

<210> 36
 <211> 3709
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (885)...(960)
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 <222> (2149)...(2260)
 <221> CDS
 <222> (3383)...(3482)

<400> 36
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 gtggctttca cttgtttatc tgtgaattga agagaagttg cttgagggtca ggcagtgtc 180
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 ctggacatag agaattgtat ttaattctta tcgcacgtcc ttgagacatg tattgtctatt 360
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 gattcaaatg caggtgtatc tctgttcagg tccagactct tctgccctga agcagtagta 480
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 tttctttgct tcccactcaa ccaggacagt tcccacgcac tttttcaaga ttcttatctg 600
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 gccaggatag gtggggaag gagtttacca catggctcgt ggggtgtgagc aactgttccc 720
 tgtccctatg gcttccact tgtggctccc accatggcct ggagttttgg gtggagtttt 780
 tcaataaaaa gccctcagca ttgcaggacg gcaagtggt gagctcttag cttcaccagg 840
 ctcatcaaag ctgctccagg aaggcccaag ccagaccaga agac atg cag atc atc 896
 Met Gln Ile Ile
 1

acc aca gcc ctg gtg tgc ttg ctg cta gct ggg atg tgg ccg gaa gat 944
 Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met Trp Pro Glu Asp
 5 10 15 20

gtg gac agc aag agc a gtgagtgtgg caggcatcat tttgcttctc tctggggagg 1000
 Val Asp Ser Lys Ser
 25

gcagaaacgt ggtcagccac tctgggggtg gagcaggctt ctctttgaac tcaccaactc 1060
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 aaggagctct gcttcatcca gacccaagga agggaacctg tgaggttact cgggtaaaagc 1240
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 agtagagtca gaaggcaaga ccgggctcta acaattggtc actottgggc aagtcacttt 1360

Sub-61

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tcttctag	tg	cag	gta	ccc	tcc	aga	tgt	tgc	tcc	tca	ttt	gcg	gag	2189
Met Gln Val Pro Phe Ser Arg Cys Cys Phe Ser Phe Ala Glu														
30 35														

caa	gag	att	ccc	ctg	agg	gca	atc	ctg	tgt	tac	aga	aat	acc	agc	tcc	2237
Gln	Glu	Ile	Pro	Leu	Arg	Ala	Ile	Leu	Cys	Tyr	Arg	Asn	Thr	Ser	Ser	
40					45					50					55	

atc	tgc	tcc	aat	gag	ggc	tta	at	gtaagtgatc	acctgctcaa	tctctcccta	2290
Ile	Cys	Ser	Asn	Glu	Gly	Leu	Ile				
60											

gagaacagaa	ccccgccagc	ctggaattac	aagagtagac	actagatgac	agtattttac	2350									
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ctctgttcac	ag	a	ttc	aag	ctg	aag	aga	ggc	aaa	gag	gcc	tgc	gcc	ttg	3419
Phe Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu															
65 70 75															

gac	aca	gtt	gga	tgg	gtt	cag	agg	cac	aga	aaa	atg	ctg	agg	cac	tgc	3467
Asp	Thr	Val	Gly	Trp	Val	Gln	Arg	His	Arg	Lys	Met	Leu	Arg	His	Cys	
			80						85						90	

ccg	tca	aaa	aga	aaa	tgagcagatt	tctttccatt	gtgggctctg	gaaaccacat	3522
Pro	Ser	Lys	Arg	Lys					
95									

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<211> 673

<212> DNA
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<220>
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<222> (67)... (450)

<400> 37

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Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala
1 5 10

aga cca ctt cat gcc ttg cag gtg ctg ctg ctt ctg tca ttg ctg ctg 156
Arg Pro Leu His Ala Leu Gln Val Leu Leu Leu Leu Ser Leu Leu Leu
15 20 25 30

act gct ctg gct tcc tcc acc aaa gga caa act aag aga aac ttg gcg 204
Thr Ala Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala
35 40 45

aaa ggc aaa gag gaa agt cta gac agt gac ttg tat gct gaa ctg cgc 252
Lys Gly Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg
50 55 60

tgc atg tgt ata aag aca acc tct gga att cat ccc aaa aac atc caa 300
Cys Met Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln
65 70 75

agt ttg gaa gtg atc ggg aaa gga acc cat tgc aac caa gtc gaa gtg 348
Ser Leu Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val
80 85 90

ata gcc aca ctg aag gat ggg agg aaa atc tgc ctg gac cca gat gct 396
Ile Ala Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala
95 100 105 110

ccc aga atc aag aaa att gta cag aaa aaa ttg gca ggt gat gaa tct 444
Pro Arg Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser
115 120 125

gct gat taatttgctc tgtttctgcc aaactctctt aactcccagg aagggtagaa 500
Ala Asp

ttttgaaacc ttgattttct agagttctca tttattcagg atacctattc ttactgtatt 560
aaaatttgga tatgtgttct attctgtctc aaaaatcaca ttttattctg agaaggttgg 620
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<210> 38
<211> 12
<212> PRT
<213> Homo sapiens

<400> 38

Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
1 5 10

<210> 39
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<212> DNA
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<220>
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 Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val Leu Ile Gly Val Gln
 10 15 20

gga acc cca gta gtg aga aag ggt cgc tgt tcc tgc atc agc acc aac 150
 Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser Cys Ile Ser Thr Asn
 25 30 35

caa ggg act atc cac cta caa tcc ttg aaa gac ctt aaa caa ttt gcc 198
 Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp Leu Lys Gln Phe Ala
 40 45 50

cca agc cct tcc tgc gag aaa att gaa atc att gct aca ctg aag aat 246
 Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile Ala Thr Leu Lys Asn
 55 60 65

gga gtt caa aca tgt cta aac cca gat tca gca gat gtg aag gaa ctg 294
 Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala Asp Val Lys Glu Leu
 70 75 80 85

att aaa aag tgg gag aaa cag gtc agc caa aag aaa aag caa aag aat 342
 Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys Lys Lys Gln Lys Asn
 90 95 100

ggg aaa aaa cat caa aaa aag aaa gtt ctg aaa gtt cga aaa tct caa 390
 Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys Val Arg Lys Ser Gln
 105 110 115

cgt tct cgt caa aag aag act aca taagagacca cttcaccaat aagtattctg 444
 Arg Ser Arg Gln Lys Lys Thr Thr
 120 125

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<210> 40
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 <212> PRT
 <213> Homo sapiens

<400> 40
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 1 5 10

<210> 41
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 41
 Glu Ile Cys Leu Asp Pro Glu Ala Pro Phe Leu Lys
 1 5 10

<210> 42
 <211> 12
 <212> PRT
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<400> 42
 Gln Val Cys Ala Asp Pro Ser Glu Glu Trp Val Gln
 1 5 10

<210> 43
 <211> 12
 <212> PRT
 <213> Homo sapiens

<400> 43
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
 1 5 10

<210> 44
 <211> 12
 <212> PRT
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<400> 44
 Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
 1 5 10

<210> 45

<211> 125
 <212> PRT
 <213> Homo sapiens

<400> 45

Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
 1 5 10 15
 Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
 20 25 30
 Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
 35 40 45
 Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
 50 55 60
 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
 65 70 75 80
 Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
 85 90 95
 Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
 100 105 110
 Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
 115 120 125

<210> 46
 <211> 128
 <212> PRT
 <213> Homo sapiens

<400> 46

Met Ser Leu Arg Leu Asp Thr Thr Pro Ser Cys Asn Ser Ala Arg Pro
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 Leu His Ala Leu Gln Val Leu Leu Leu Ser Leu Leu Leu Thr Ala
 20 25 30
 Leu Ala Ser Ser Thr Lys Gly Gln Thr Lys Arg Asn Leu Ala Lys Gly
 35 40 45
 Lys Glu Glu Ser Leu Asp Ser Asp Leu Tyr Ala Glu Leu Arg Cys Met
 50 55 60
 Cys Ile Lys Thr Thr Ser Gly Ile His Pro Lys Asn Ile Gln Ser Leu
 65 70 75 80
 Glu Val Ile Gly Lys Gly Thr His Cys Asn Gln Val Glu Val Ile Ala
 85 90 95
 Thr Leu Lys Asp Gly Arg Lys Ile Cys Leu Asp Pro Asp Ala Pro Arg
 100 105 110
 Ile Lys Lys Ile Val Gln Lys Lys Leu Ala Gly Asp Glu Ser Ala Asp
 115 120 125

<210> 47
 <211> 96
 <212> PRT
 <213> Homo sapiens

<400> 47

Met Gln Ile Ile Thr Thr Ala Leu Val Cys Leu Leu Leu Ala Gly Met
 1 5 10 15
 Trp Pro Glu Asp Val Asp Ser Lys Ser Met Gln Val Pro Phe Ser Arg
 20 25 30
 Cys Cys Phe Ser Phe Ala Glu Gln Glu Ile Pro Leu Arg Ala Ile Leu
 35 40 45
 Cys Tyr Arg Asn Thr Ser Ser Ile Cys Ser Asn Glu Gly Leu Ile Phe
 50 55 60
 Lys Leu Lys Arg Gly Lys Glu Ala Cys Ala Leu Asp Thr Val Gly Trp
 65 70 75 80
 Val Gln Arg His Arg Lys Met Leu Arg His Cys Pro Ser Lys Arg Lys

Pub 61

85

90

95

<210> 48
<211> 93
<212> PRT
<213> Homo sapiens

<400> 48

Met	Lys	Ile	Ser	Val	Ala	Ala	Ile	Pro	Phe	Phe	Leu	Leu	Ile	Thr	Ile
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Ala	Leu	Gly	Thr	Lys	Thr	Glu	Ser	Ser	Ser	Arg	Gly	Pro	Tyr	His	Pro
			20					25					30		
Ser	Glu	Cys	Cys	Phe	Thr	Tyr	Thr	Thr	Tyr	Lys	Ile	Pro	Arg	Gln	Arg
		35					40					45			
Ile	Met	Asp	Tyr	Tyr	Glu	Thr	Asn	Ser	Gln	Cys	Ser	Lys	Pro	Gly	Ile
	50					55					60				
Val	Phe	Ile	Thr	Lys	Arg	Gly	His	Ser	Val	Cys	Thr	Asn	Pro	Ser	Asp
65					70					75					80
Lys	Trp	Val	Gln	Asp	Tyr	Ile	Lys	Asp	Met	Lys	Glu	Asn			
				85					90						

<210> 49
<211> 93
<212> PRT
<213> Homo sapiens

<400> 49

Met	Gln	Val	Ser	Thr	Ala	Ala	Leu	Ala	Val	Leu	Leu	Cys	Thr	Met	Ala
1				5					10					15	
Leu	Cys	Asn	Gln	Val	Leu	Ser	Ala	Pro	Leu	Ala	Ala	Asp	Thr	Pro	Thr
			20					25					30		
Ala	Cys	Cys	Phe	Ser	Tyr	Thr	Ser	Arg	Gln	Ile	Pro	Gln	Asn	Phe	Ile
		35					40					45			
Ala	Asp	Tyr	Phe	Glu	Thr	Ser	Ser	Gln	Cys	Ser	Lys	Pro	Ser	Val	Ile
	50					55					60				
Phe	Leu	Thr	Lys	Arg	Gly	Arg	Gln	Val	Cys	Ala	Asp	Pro	Ser	Glu	Glu
65					70					75					80
Trp	Val	Gln	Lys	Tyr	Val	Ser	Asp	Leu	Glu	Leu	Ser	Ala			
					85				90						

<210> 50
<211> 98
<212> PRT
<213> Homo sapiens

<400> 50

Met	Lys	Val	Ser	Ala	Val	Leu	Leu	Cys	Leu	Leu	Leu	Met	Thr	Ala	Ala
1				5					10					15	
Phe	Asn	Pro	Gln	Gly	Leu	Ala	Gln	Pro	Asp	Ala	Leu	Asn	Val	Pro	Ser
			20					25					30		
Thr	Cys	Cys	Phe	Thr	Phe	Ser	Ser	Lys	Lys	Ile	Ser	Leu	Gln	Arg	Leu
		35					40					45			
Lys	Ser	Tyr	Val	Ile	Thr	Thr	Ser	Arg	Cys	Pro	Gln	Lys	Ala	Val	Ile
	50					55					60				
Phe	Arg	Thr	Lys	Leu	Gly	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Glu	Lys
65					70					75					80
Trp	Val	Gln	Asn	Tyr	Met	Lys	His	Leu	Gly	Arg	Lys	Ala	His	Thr	Leu
				85					90					95	

Lys Thr

<210> 51

217 61
<211> .889
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (54) ... (344)

<400> 51

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Lys Val Ser Ala Ala Leu Leu Trp Leu Leu Leu Ile Ala Ala Ala Phe
5 10 15

agc ccc cag ggg ctc gct ggg cca gct tct gtc cca acc acc tgc tgc 152
Ser Pro Gln Gly Leu Ala Gly Pro Ala Ser Val Pro Thr Thr Cys Cys
20 25 30

ttt aac ctg gcc aat agg aag ata ccc ctt cag cga cta gag agc tac 200
Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser Tyr
35 40 45

agg aga atc acc agt ggc aaa tgt ccc cag aaa gct gtg atc ttc aag 248
Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe Lys
50 55 60 65

acc aaa ctg gcc aag gat atc tgt gcc gac ccc aag aag aag tgg gtg 296
Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp Val
70 75 80

cag gat tcc atg aag tat ctg gac caa aaa tct cca act cca aag cca 344
Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys Pro
85 90 95

taaataatca ccatttttga aaccaaacca gagcctgagt gttgcctaatt ttgttttccc 404
ttcttacaat gcattctgag gtaacctcat tatcagtgcca aagggcatgg gttttattat 464
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<210> 52
<211> 114
<212> PRT
<213> Homo sapiens

<400> 52

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Ser Leu Cys Ala Leu Leu Val Leu Leu Leu Leu Leu Thr Gln Pro Gly
20 25 30
Pro Ile Ala Ser Ala Gly Pro Ala Ala Val Leu Arg Glu Leu Arg
35 40 45
Cys Val Cys Leu Gln Thr Thr Gln Gly Val His Pro Lys Met Ile Ser
50 55 60
Asn Leu Gln Val Phe Ala Ile Gly Pro Gln Cys Ser Lys Val Glu Val

65 70 75 80
 Val Ala Ser Leu Lys Asn Gly Lys Glu Ile Cys Leu Asp Pro Glu Ala
 85 90 95
 Pro Phe Leu Lys Lys Val Ile Gln Lys Ile Leu Asp Gly Gly Asn Lys
 100 105 110
 Glu Asn

<210> 53
 <211> 107
 <212> PRT
 <213> Homo sapiens

<400> 53
 Met Ala Arg Ala Thr Leu Ser Ala Ala Pro Ser Asn Pro Arg Leu Leu
 1 5 10 15
 Arg Val Ala Leu Leu Leu Leu Val Ala Ala Ser Arg Arg Ala
 20 25 30
 Ala Gly Ala Pro Leu Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35 40 45
 Leu Gln Gly Ile His Leu Lys Asn Ile Gln Ser Val Lys Val Lys Ser
 50 55 60
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65 70 75 80
 Gly Gln Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys Lys Ile
 85 90 95
 Ile Glu Lys Met Leu Lys Asn Gly Lys Ser Asn
 100 105

<210> 54
 <211> 98
 <212> PRT
 <213> Homo sapiens

<400> 54
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 1 5 10 15
 Ser Gly Thr Gln Gly Ile Pro Leu Ala Arg Thr Val Arg Cys Asn Cys
 20 25 30
 Ile His Ile Asp Asp Gly Pro Val Arg Met Arg Ala Ile Gly Lys Leu
 35 40 45
 Glu Ile Ile Pro Ala Ser Leu Ser Cys Pro Arg Val Glu Ile Ile Ala
 50 55 60
 Thr Met Lys Lys Asn Asp Glu Gln Arg Cys Leu Asn Pro Glu Ser Lys
 65 70 75 80
 Thr Ile Lys Asn Leu Met Lys Ala Phe Ser Gln Lys Arg Ser Lys Arg
 85 90 95
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<210> 55
 <211> 1041
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (18)...(338)

<400> 55
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 Met Ala Arg Ala Ala Leu Ser Ala Ala Pro Ser

50

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Asn Pro Arg Leu Leu Arg Val Ala Leu Leu Leu Leu Leu Leu Val Ala	15	20	25	
gct ggc cgg cgc gca gca gga gcg tcc gtg gcc act gaa ctg cgc tgc				146
Ala Gly Arg Arg Ala Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys	30	35	40	
cag tgc ttg cag acc ctg cag gga att cac ccc aag aac atc caa agt				194
Gln Cys Leu Gln Thr Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser	45	50	55	
gtg aac gtg aag tcc ccc gga ccc cac tgc gcc caa acc gaa gtc ata				242
Val Asn Val Lys Ser Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile	60	65	70	75
gcc aca ctc aag aat ggg cgg aaa gct tgc ctc aat cct gca tcc ccc				290
Ala Thr Leu Lys Asn Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro	80	85	90	
ata gtt aag aaa atc atc gaa aag atg ctg aac agt gac aaa tcc aac				338
Ile Val Lys Lys Ile Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn	95	100	105	
tgaccagaag ggaggaggaa gctcactggt ggctgttcct gaaggaggcc ctgcccttat				398
aggaacagaa gaggaagag agacacagct gcagaggcca cctggattgt gcctaattgtg				458
tttgagcatc gcttaggaga agtcttctat ttattttattt attcattagt tttgaagatt				518
ctatgttaat atttttaggtg taaaataatt aagggtatga ttaactctac ctgcacactg				578
tcctattata ttcattcttt ttgaaatgtc aaccccaagt tagttcaatc tggattcata				638
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gagcctgcaa catgccagcc actgtgatag aggctggcgg atccaagcaa atggccaatg				758
agatcattgt gaaggcaggg gaatgtatgt gcacatctgt tttgtaactg tttagatgaa				818
tgtcagttgt tattttattga aatgatttca cagtgtgtgg tcaacatttc tcatgttgaa				878
actttaagaa ctaaaatgtt ctaaaatatcc cttggacatt ttatgtcttt cttgtaaggc				938
atactgcctt gtttaatggt agttttacag tgtttctggc ttagaacaaa ggggcttaat				998
tattgatgtt ttcatagaga atataaaaat aaagcactta tag				1041

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Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys	1	5	10	15
Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys	20	25	30	
Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys	35	40	45	
Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln	50	55	60	
Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met	65	70	75	80
	85	90		

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Sub G1

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 Ala Gly Ala Ser Val Ala Thr Glu Leu Arg Cys Gln Cys Leu Gln Thr
 35 40 45
 Leu Gln Gly Ile His Pro Lys Asn Ile Gln Ser Val Asn Val Lys Ser
 50 55 60
 Pro Gly Pro His Cys Ala Gln Thr Glu Val Ile Ala Thr Leu Lys Asn
 65 70 75 80
 Gly Arg Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys Lys Ile
 85 90 95
 Ile Glu Lys Met Leu Asn Ser Asp Lys Ser Asn
 100 105

<210> 58
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 Met Thr Ser Lys Leu
 1 5
 gcc gtg gct ctc ttg gca gcc ttc ctg att tct gca gct ctg tgt gaa 164
 Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser Ala Ala Leu Cys Glu
 10 15 20
 ggt gca gtt ttg cca agg agt gct aaa gaa ctt aga tgt cag tgc ata 212
 Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu Arg Cys Gln Cys Ile
 25 30 35
 aag aca tac tcc aaa cct ttc cac ccc aaa ttt atc aaa gaa ctg aga 260
 Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe Ile Lys Glu Leu Arg
 40 45 50
 gtg att gag agt gga cca cac tgc gcc aac aca gaa att att gta aag 308
 Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr Glu Ile Ile Val Lys
 55 60 65
 ctt tct gat gga aga gag ctc tgt ctg gac ccc aag gaa aac tgg gtg 356
 Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro Lys Glu Asn Trp Val
 70 75 80 85
 cag agg gtt gtg gag aag ttt ttg aag agg gct gag aat tca 398
 Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala Glu Asn Ser
 90 95
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 caaatctact tcaacacttc atgtattgtg tgggtctgtt gtagggttgc cagatgcaat 518
 acaagattcc tgggttaaatt tgaatttcag taaacaatga atagtgtttc attgtaccat 578
 gaaatatcca gaacatactt atatgtaaag tattatttat ttgaatctac aaaaaacaac 638
 aaataatttt taaatataag gattttccta gatattgcac gggagaatat acaaatagca 698
 aaattgggcc aagggccaaag agaatatccg aactttaatt tcaggaattg aatgggtttg 758
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 aaaaagtatt agccaccatc ttacctcaca gtgatgttgt gaggacatgt ggaagcactt 998
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 cattgattga atagttataa agatgttata gttaaatttat tttatttttag atattaaatg 1178
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 gtttatctga aattttaatt gaactaacia tcctagtttg atactoccag tcttgtcatt 1358
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 agccaaaact ccacagtcaa tattagtaat ttcttgctgg ttgaaacttg tttattatgt 1478
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 ttttaacttt aaaaaaaccc gg 1560

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 1 5 10 15

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 <212> PRT
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<400> 60
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 1 5 10

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 <212> PRT
 <213> Homo sapiens

<400> 61
 Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val
 1 5 10 15

<210> 62
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 <212> PRT
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<400> 62
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<210> 63
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<400> 63
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<210> 64
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Sub-61

<213> Homo sapiens
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<211> 12
<212> PRT
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<211> 12
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Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln
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Glu Ile Cys Ala Asp Pro Lys Glu Arg Trp Val Arg
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Met Ile Cys Ala Asp Pro Lys Xaa Ala Ala Xaa Ala Ala Trp Val Gln
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1 5 10 15
<210> 70
<211> 15
<212> PRT
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<210> 71
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<212> .PRT
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<400> 71
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<210> 72
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<400> 72
Lys Ala Cys Leu Asn Pro Ala Ser Pro Ile Val Lys
1 5 10

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<400> 73
Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Lys
1 5 10

<210> 74
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<400> 74
Lys Ala Cys Leu Asn Pro Ala Ser Pro Met Val Gln
1 5 10

<210> 75
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<400> 75
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1 5 10

<210> 76
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<212> DNA
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ctg tgc ctg ctg ctc ata gca gcc acc ttc att ccc caa ggg ctc gct 100
Leu Cys Leu Leu Leu Ile Ala Ala Thr Phe Ile Pro Gln Gly Leu Ala
10 15 20

cag cca gat gca atc aat gcc cca gtc acc tgc tgc tat aac ttc acc 148

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Gln	Pro	Asp	Ala	Ile	Asn	Ala	Pro	Val	Thr	Cys	Cys	Tyr	Asn	Phe	Thr		
	25					30					35						
aat	agg	aag	atc	tca	gtg	cag	agg	ctc	gcg	agc	tat	aga	aga	atc	acc	196	
Asn	Arg	Lys	Ile	Ser	Val	Gln	Arg	Leu	Ala	Ser	Tyr	Arg	Arg	Ile	Thr		
40					45					50					55		
agc	agc	aag	tgt	ccc	aaa	gaa	gct	gtg	atc	ttc	aag	acc	att	gtg	gcc	244	
Ser	Ser	Lys	Cys	Pro	Lys	Glu	Ala	Val	Ile	Phe	Lys	Thr	Ile	Val	Ala		
				60					65					70			
aag	gag	atc	tgt	gct	gac	ccc	aag	cag	aag	tgg	ggt	cag	gat	tcc	atg	292	
Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Gln	Lys	Trp	Val	Gln	Asp	Ser	Met		
		75						80					85				
gac	cac	ctg	gac	aag	caa	acc	caa	act	ccg	aag	act	tga	acactcactc			341	
Asp	His	Leu	Asp	Lys	Gln	Thr	Gln	Thr	Pro	Lys	Thr	*					
		90						95									
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		Met Asn Ala	Lys Val Val	Val Val Val	Leu Val Leu												
		1		5	10												
gtg ctg acc	gcg ctc	tgc ctc	agc gac	ggg aag	ccc gtc	agc ctg	agc	160									
Val Leu Thr	Ala Leu	Cys Leu	Ser Asp	Gly Lys	Pro Val	Ser Leu	Ser										
	15		20		25												
tac aga tgc	cca tgc	cga ttc	ttc gaa	agc cat	ggt gcc	aga gcc	aac	208									
Tyr Arg Cys	Pro Cys	Arg Phe	Phe Glu	Ser His	Val Ala	Arg Ala	Asn										
	30		35		40												
gtc aag cat	ctc aaa	att ctc	aac act	cca aac	tgt gcc	ctt cag	att	256									
Val Lys His	Leu Lys	Ile Leu	Asn Thr	Pro Asn	Cys Ala	Leu Gln	Ile										
	45		50		55												
gta gcc cgg	ctg aag	aac aac	aac aga	caa gtc	tgc att	gac ccg	aag	304									
Val Ala Arg	Leu Lys	Asn Asn	Asn Arg	Gln Val	Cys Ile	Asp Pro	Lys										
	60		65		70		75										
cta aag tgg	att cag	gag tac	ctg gag	aaa gct	tta aac	aag		346									
Leu Lys Trp	Ile Gln	Glu Tyr	Leu Glu	Lys Ala	Leu Asn	Lys											
	80		85														
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Sub 61

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gtgtggggtg	ggcaccattga	tctgggatcg	ggcctgaggt	ttgcagcatt	tagaccctgc	526
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caagcagtta	gttccttcat	gatcatcaca	atcatcatca	ttctcattct	catttttttaa	706
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cattttttta	tatatatttt	tgtgcacatt	tttttttacg	attctttaga	aaacaaatgt	1606
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			1								5					
gtc	atc	ctc	att	gct	act	gcc	ctc	tgc	gct	cct	gca	tct	gcc	tcc	cca	101
Val	Ile	Leu	Ile	Ala	Thr	Ala	Leu	Cys	Ala	Pro	Ala	Ser	Ala	Ser	Pro	
10					15					20					25	
tat	tcc	tcg	gac	acc	aca	ccc	tgc	tgc	ttt	gcc	tac	att	gcc	cgc	cca	149
Tyr	Ser	Ser	Asp	Thr	Thr	Pro	Cys	Cys	Phe	Ala	Tyr	Ile	Ala	Arg	Pro	
				30					35						40	
ctg	ccc	cgt	gcc	cac	atc	aag	gag	tat	ttc	tac	acc	agt	ggc	aag	tgc	197
Leu	Pro	Arg	Glu	Ala	His	Ile	Lys	Glu	Tyr	Phe	Tyr	Thr	Ser	Gly	Lys	Cys
			45					50					55			
tcc	aac	cca	gca	gtc	gtc	ttt	gtc	acc	cga	aag	aac	cgc	caa	gtg	tgt	245
Ser	Asn	Pro	Ala	Val	Val	Phe	Val	Thr	Arg	Lys	Asn	Arg	Gln	Val	Cys	
			60				65						70			
gcc	aac	cca	gag	aag	aaa	tgg	gtt	cgg	gag	tac	atc	aac	tct	ttg	gag	293
Ala	Asn	Pro	Glu	Lys	Lys	Trp	Val	Arg	Glu	Tyr	Ile	Asn	Ser	Leu	Glu	
			75				80				85					
atg	agc	taggatggag	agtccttgaa	cctgaactta	cacaaatttg	cctgtttctg										349
Met	Ser															

90

cttgcctcttg tcttagcttg ggaggcttcc cctcactatc ctaccccacc cgtccttga 409
 agggcccaga ttctgaccac gacgagcagc agttacaaaa accttcccca ggctggacgt 469
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 Met Lys Leu
 1

tgc gtg act gtc ctg tct ctc ctc atg cta gta gct gcc ttc tgc tct 165
 Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala Phe Cys Ser
 5 10 15

cca gcg ctc tca gca cca atg ggc tca gac cct ccc acc gcc tgc tgc 213
 Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr Ala Cys Cys
 20 25 30 35

ttt tct tac acc gcg agg aag ctt cct cgc aac ttt gtg gta gat tac 261
 Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val Val Asp Tyr
 40 45 50

tat gag acc agc agc ctc tgc tcc cag cca gct gtg gta ttc caa acc 309
 Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val Phe Gln Thr
 55 60 65

aaa aga agc aag caa gtc tgt gct gat ccc agt gaa tcc tgg gtc cag 357
 Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser Trp Val Gln
 70 75 80

gag tac gtg tat gac ctg gaa ctg aac tgagctgctc agagacagga 404
 Glu Tyr Val Tyr Asp Leu Glu Leu Asn
 85 90

agtcttcagg gaaggtcacc tgagcccagg tgctttctcca tgagacacat ctctccata 464
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 ctatggggat ggtccactgt cactgtttct ctgctgttgc aaatacatgg ataacacatt 644
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Pub-G1

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<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (123)... (353)

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tt gct cag cca gat tca gtt tcc att cca atc acc tgc tgc ttt aac      167
Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn
  1          5          10          15

gtg atc aat agg aaa att cct atc cag agg ctg gag agc tac aca aga      215
Val Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg
          20          25          30

atc acc aac atc caa tgt ccc aag gaa gct gtg atc ttc aag acc caa      263
Ile Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Gln
          35          40          45

cgg ggc aag gag gtc tgt gct gac ccc aag gag aga tgg gtc agg gat      311
Arg Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp
          50          55          60

tcc atg aag cat ctg gac caa ata ttt caa aat ctg aag cca      353
Ser Met Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
          65          70          75

tgagccttca tacatggact gagagtcaga gcttgaagaa aagcttattt attttcccca      413
acctccccc ggtgcagtgt gacattattt tattataaca tccacaaaga gattattttt      473
aaataattta aagcataata tttcttaaaa agtatttaat tatattttaag ttgttgatgt      533
tttaactcta tctgtcatat atcctagtga atgtaaaatg caaaatcctg gtgatgtgtt      593
ttttgttttt gttttcctgt gagctcaact aagttcacgg caaaatgtca ttgttctccc      653
tcctacctgt ctgtagtggt gtggggctct cccatggatc atcaaggtga aacactttgg      713
tattctttgg caatcagtg cctgtgaagt caaatgtgtg ctttgtactg ctgttggtga      773
aattgatgtt actgtatata actatggaat ttgtaaaaaa aatttcaaaa agaaaaaaat      833
atatataatt taaaactaag aaaaaaaaaa aaaaaaaaaa aaaaagggtt ctattgactt      893
gggttaatcg tgtgaccgcg gtggctggca cgaattgac caacctgggg gttagtagatg      953
cttagttaaa ctttcgttta ttgctaagg ttaactactg ctgtttcccg tggggggtgtg      1013
gctaggctaa gcgttttgag ctgcattgct gcgtgcttga tgcctgtccc ttttgatcgt      1073
ggtgatttag agggatgaact cactggaatg gggatgcttg catgtgtaat cttactaaga      1133
gctaatagaa aggctaggac caaaccagaa acctcgaatt ctcatgtgga agcccatgcc      1193
ctcaccctcc aacatgaaag cctctgcagc acttctgtgt ctgctgctca cagcagctgc      1253
tttcagcccc caggggcttg ctccagcagt tgggattaat acttcaacta cctgctgcta      1313
cagatttatc aataagaaaa tccctaagca gaggctggag agctacagaa ggaccaccag      1373
tagccactgt ccccggaag ctgtaattct caagaccaaa ctggacaagg agatctgtgc      1433
tgacccca cagaagtggg tccaggactt tatgaagcac ctggacaaga aaacccaaac      1493
tccaaagctt tgaacattca tgactgaact gaaaacaagc catgacttga gaaacaaata      1553
atttgatata cctgtccttt ctccagagtgg ttctgagatt attttaatct aattctaagg      1613
aatatgagct ttatgtaata atgtgaatca tgggttttct tagtagattt taaaagttat      1673
taatatttta atttaattct ccatggattt tgggtgggtt tgaacataaa gccttggatg      1733
tatatgtcat ctccagtctg taaaaactgt gggatgctcc tcccttctct acctcatggg      1793
ggtattgtat aagtccttgc aagaatcagt gcaaagattt gctttaattg ttaagatatg      1853
atgtccctat ggaagcatat tggtattata taattacata ttgcatatg tatgactccc      1913
aaattttcac ataaaaataga tttttgtata acaaaaaaaa aaaaaaaa aaggacacgg      1973
gcagcagaca gtggtcagtc ctttcttggc tctgctgaca ctgagccca cattccgtca      2033
cctgctcaga atcatgcagg tctccactgc tgcccttget gtctctctct gcaccatggc      2093
tctctgcaac cagttctctg catcacttgc tgctgacacg ccgaccgctt gctgcttcag      2153

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Sub-61

ctacacctcc	cggcagattc	cacagaattt	catagctgac	tactttgaga	cgagcagcca	2213
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cagtgaggag	tgggtccaga	aatatgtcag	cgacctggag	ctgagtgcct	gaggggtcca	2333
gaagcttcga	ggcccagcga	cctcgggtggg	cccagtgagg	aggagcagga	gcctgagcct	2393
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ccacactgtg	ggactcttct	taacttaaat	tttaatttat	ttatactatt	tagtttttgt	2513
aatttatatt	cgatttcaca	gtgtgtttgt	gattgtttgc	tctgagagtt	cccctgtccc	2573
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gcagtcattg	caocaaagcc	accagactga	caaattgtga	tcggatgctt	ttgttcaggg	2693
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<210> 81
 <211> 1085
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (329) ... (625)

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tcccgtgggg	gtgtggctag	gctaagcgtt	ttgagctgca	ttgctgcgtg	cttgatgctt	180
gtcccttttg	atcgtggtga	tttagagggt	gaactcactg	gaatggggat	gcttgcattg	240
gtaattctac	taagagctaa	tagaagggt	aggaccaaac	cagaaacctc	caattctcat	300
gtggaagccc	atgcctcac	cctccaac	atg aaa gcc tct gca gca ctt ctg			352

Met Lys Ala Ser Ala Ala Leu Leu
 1 5

tgt ctg ctg ctc aca gca gct gct ttc agc ccc cag ggg ctt gct cag	400
Cys Leu Leu Leu Thr Ala Ala Ala Phe Ser Pro Gln Gly Leu Ala Gln	
10 15 20	

cca gtt ggg att aat act tca act acc tgc tgc tac aga ttt atc aat	448
Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn	
25 30 35 40	

aag aaa atc cct aag cag agg ctg gag agc tac aga agg acc acc agt	496
Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser	
45 50 55	

agc cac tgt ccc cgg gaa gct gta atc ttc aag acc aaa ctg gac aag	544
Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu Asp Lys	
60 65 70	

gag atc tgt gct gac ccc aca cag aag tgg gtc cag gac ttt atg aag	592
Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe Met Lys	
75 80 85	

cac ctg gac aag aaa acc caa act cca aag ctt tgaacattca tgactgaact	645
His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu	
90 95	

gaaaacaagc	catgacttga	gaaacaaata	atttgtatac	cctgtccttt	ctcagagtgg	705
ttctgagatt	attttaattc	aattctaagg	aatatgagct	ttatgtaata	atgtgaatca	765
tggtttttct	tagtagattt	taaaagttat	taatatttta	atttaattct	ccatggattt	825
tgggtgggtt	tgaacataaa	gccttggtat	tatatgtcat	ctcagtgtct	taaaaactgt	885
gggatgtccc	tcccttctct	acctcatggg	ggtattgtat	aagtccttgc	aagaatcagt	945
gcaaagattt	gctttaattg	tttaagatat	atgtccctat	ggaagcatat	tggtattata	1005
taattacata	tttgcatatg	tatgactccc	aaattttcac	ataaaataga	tttttgtata	1065
acaaaaaaaa	aaaaaaaaaa					1085

Sub C1
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<211> 775
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (84)...(359)

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Met Gln Val Ser Thr Ala Ala Leu Ala Val
1 5 10
ctc ctc tgc acc atg gct ctc tgc aac cag ttc tct gca tca ctt gct 161
Leu Leu Cys Thr Met Ala Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala
15 20 25
gct gac acg ccg acc gcc tgc tgc ttc agc tac acc tcc cgg cag att 209
Ala Asp Thr Pro Thr Ala Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile
30 35 40
cca cag aat ttc ata gct gac tac ttt gag acg agc agc cag tgc tcc 257
Pro Gln Asn Phe Ile Ala Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser
45 50 55
aag ccc ggt gtc atc ttc cta acc aag cga agc cgg cag gtc tgt gct 305
Lys Pro Gly Val Ile Phe Leu Thr Lys Arg Ser Arg Gln Val Cys Ala
60 65 70
gac ccc agt gag gag tgg gtc cag aaa tat gtc agc gac ctg gag ctg 353
Asp Pro Ser Glu Glu Trp Val Gln Lys Tyr Val Ser Asp Leu Glu Leu
75 80 85 90
agt gcc tgaggggtcc agaagcttcg aggccacgcg acctcggtgg gccagtgagg 409
Ser Ala
gaggagcagg agcctgagcc ttgggaacat gctgtgtgacc tccacagcta cctcttctat 469
ggactgggtg ttgccaaaca gccacactgt ggcactcttc ttaacttaaa ttttaattta 529
tttatactat ttagtttttg taatttattt tctgatttcac agtgtgtttg tgattgtttg 589
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aaaggt 775

<210> 83
<211> 98
<212> PRT
<213> Homo sapiens

<400> 83
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Phe Asn Pro Gln Gly Leu Ala Gln Pro Asp Ala Leu Asn Val Pro Ser
20 25 30
Thr Cys Cys Phe Thr Phe Ser Ser Lys Lys Ile Ser Leu Gln Arg Leu
35 40 45
Lys Ser Tyr Val Ile Thr Thr Ser Arg Cys Pro Gln Lys Ala Val Ile
50 55 60
Phe Arg Thr Lys Leu Gly Lys Glu Ile Cys Ala Asp Pro Lys Glu Lys

65 70 75 80
 Trp Val Gln Asn Tyr Met Lys His Leu Gly Arg Lys Ala His Thr Leu
 85 90 95

Lys Thr

<210> 84
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A region within a peptide of a chemokine, a variant, or a derivative thereof.

<221> SITE
 <222> 1
 <223> Xaa is Ala or Leu.

<221> SITE
 <222> 4
 <223> Xaa is Lys, Ser or Thr.

<221> SITE
 <222> 5
 <223> Xaa is any amino acid.

<221> SITE
 <222> 6
 <223> Xaa is Lys, Glu, Ser or Arg.

<221> SITE
 <222> 8
 <223> Xaa is Val or Ile.

<400> 84
 Xaa Asp Pro Xaa Xaa Xaa Trp Xaa Gln
 1 5

<210> 85
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> A chemokine variant.

<400> 85
 Cys Leu Asp Pro Lys Gln Lys Trp Ile Gln
 1 5 10